Very Fast Kinetics

- What is "very fast?"
 - Stopped flow methods: 1+ ms⁻¹ rates
 - What about 10-100 μ s⁻¹ rates?

• Examples:

- Very fast protein folding
- pH neutralization
- Some ion binding (e.g. Ca²⁺)

Fluctuation Methods

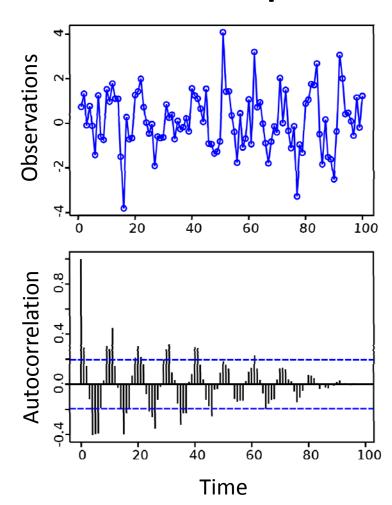
- Idea: Measure some quantity as it changes over time
 - System is at equilibrium, but changes still occur
 - Fluctuations will reflect kinetics

Challenges:

- Need sensitive equipment to measure small changes
- Need a system that is theoretically (and practically) tractable

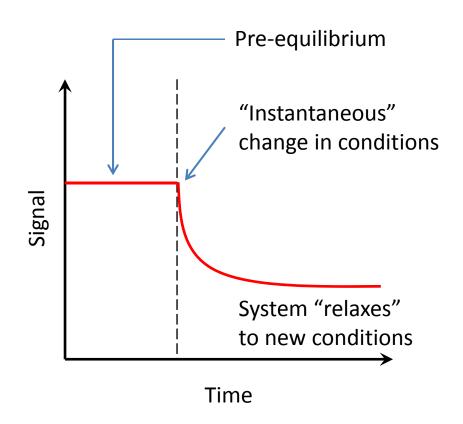
Fluctuation Methods: Examples

- Methods
 - Refractive index
 - Concentration
 - Light scattering
 - Pressure
- Autocorrelation: how an observed quantity correlates to itself (typically over time)

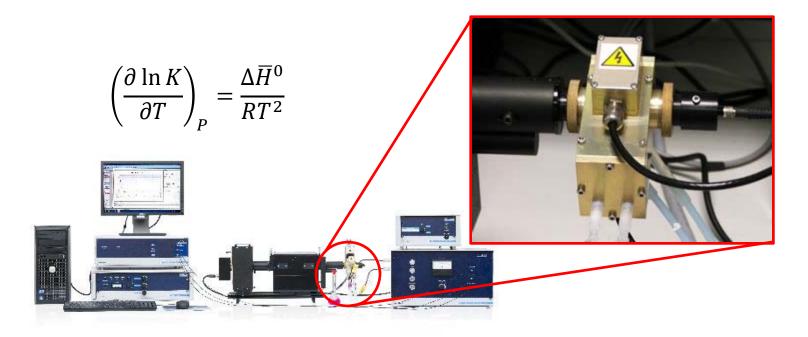


Relaxation/Perturbation Methods

- Idea: Start at equilibrium, then change conditions (no new intermediates)
- New equilibrium will be established → observe change over time
- Critical: Kinetics will reflect <u>new</u> conditions, not old conditions

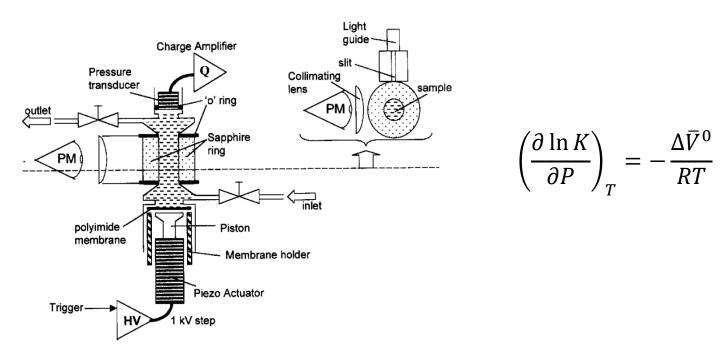


Method 1: Temperature Jump



 Electrical discharge, laser pulse rapidly increases temperature (small sample volume)

Method 2: Pressure Jump



- Diaphragm bursts to increase (or decrease) pressure of system
- To keep change in K small, $\Delta P \approx 10^2 10^3$ atm

Method 3: Flash Photolysis

Scheme 1. Proposed Reaction Mechanism for Photolysis of 1-(2-Nitrophenyl)ethyl Sulfate¹⁴

Me
$$OSO_3^ hv$$
 $OSO_3^ -H^+$ $OSO_3^ OSO_3^ OSO_3^-$

- Rapid flash of light (or laser pulse) releases H+ to change pH
- Other "caged" molecules exist (e.g. ATP)

Relaxation Kinetics Example

• Binding reaction:

$$A + B \underset{k_{-1}}{\overset{k_1}{\rightleftarrows}} P$$

Why Can We Ignore x^2 ?

- Consider equilibrium:
 - Let $A_{eq} = 10 \text{ mM}$ and $B_{eq} = 50 \text{ mM}$
 - If small perturbation, x is 1 mM

• Then:

$$-A_{eq}B_{eq} = 500 \text{ mM}^2$$

$$-(A_{eq} + B_{eq})x = 60 \text{ mM}^2$$

$$-x^2 = 1 \text{ mM}^2$$

This is much smaller than the other two

Implications of Relaxation Kinetics

 Remember kinetic rates (and equilibrium) concentrations are from <u>new</u> conditions!!

• Curves will always be exponential, because x^2 will <u>always</u> be small if perturbation is small

• Determining τ at multiple conditions (e.g. A_{eq} , B_{eq} and P_{eq}) can reveal rate constants

Relaxation Time Constants

TABLE 7.4 Relaxation Times for Reactions Involving Single Steps	
Mechanism	Relaxation time*
$A \rightleftharpoons B$ k_{-1} $A + B \rightleftharpoons P$ k_{-1} $A + B + C \rightleftharpoons P$ k_{-1} $A + B \rightleftharpoons P + Q$ k_{-1} $2A \rightleftharpoons A_{2}$	$ au \equiv rac{1}{k_1 + k_{-1}}$ $ au \equiv rac{1}{k_{-1} + k_1([\overline{A}] + [\overline{B}])}$ $ au \equiv rac{1}{k_{-1} + k_1([\overline{A}][\overline{B}] + [\overline{B}][\overline{C}] + [\overline{A}][\overline{C}])}$ $ au \equiv rac{1}{k_{-1} + k_1([\overline{A}][\overline{B}] + [\overline{B}][\overline{C}] + [\overline{A}][\overline{C}])}$ $ au \equiv rac{1}{k_1([\overline{A}] + [\overline{B}]) + k_{-1}([\overline{P}] + [\overline{Q}])}$
$ZA \leftarrow A_2$ k_{-1}	$ au = rac{1}{4k_1[\overline{f A}] + k_{-1}}$

^{*[}A], [B], etc., represent the equilibrium concentrations after the perturbation. Source: M. Eigen and L. De Maeyer, in *Investigation of Rates and Mechanisms of Reactions*, 3d ed., vol. 6, part 2, ed. G. G. Hammes (New York: Wiley-Interscience, 1974), chapter 3.

Example: Dimerization Kinetics in DNA

Dimerization scheme:

$$2A \underset{k_{-1}}{\overset{k_1}{\rightleftarrows}} A_2$$

Time constant:

$$\tau = \frac{1}{4k_1 A_{eq} + k_{-1}}$$

Modified time constant:

$$\frac{1}{\tau^2} = k_{-1}^2 + 8k_1k_{-1}A_{total}$$

Strategy: Relaxation Kinetics

- For individual points (to determine τ):
 - Always first-order kinetics (exponential)
 - Plot $\ln[A]$ vs. $t \rightarrow$ slope will be $\pm \frac{1}{\tau}$
- Determine how τ varies with A_{eq} , B_{eq} , etc.
 - Figure out how to linearize the function to relate slope, intercept to kinetic parameters
- Remember: Linearization is <u>bad</u> for real-life situations; use nonlinear least squares